



## SEQUENCE LISTING

<110> Houston, Michael E.  
Hodges, Robert

<120> Use of Coiled-Coil Structural Scaffold to Generate  
Structure-Specific Peptides

<130> 003592-007

<150> US 60/211,892

<151> 2000-06-14

<150> US 60/213,387

<151> 2000-06-23

<160> 17

<170> PatentIn version 3.0

<210> 1

<211> 619

<212> PRT

<213> Streptococcus pneumoniae

<400> 1

Met	Asn	Lys	Lys	Lys	Met	Ile	Leu	Thr	Ser	Leu	Ala	Ser	Val	Ala	Ile
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Leu	Gly	Ala	Gly	Phe	Val	Ala	Ser	Gln	Pro	Thr	Val	Val	Arg	Ala	Glu
			20					25					30		
Glu	Ser	Pro	Val	Ala	Ser	Gln	Ser	Lys	Ala	Glu	Lys	Asp	Tyr	Asp	Ala
		35					40					45			
Ala	Lys	Lys	Asp	Ala	Lys	Asn	Ala	Lys	Lys	Ala	Val	Glu	Asp	Ala	Gln
		50				55					60				
Lys	Ala	Leu	Asp	Asp	Ala	Lys	Ala	Ala	Gln	Lys	Lys	Tyr	Asp	Glu	Asp
65					70				75					80	
Gln	Lys	Lys	Thr	Glu	Glu	Lys	Ala	Ala	Leu	Glu	Lys	Ala	Ala	Ser	Glu
			85						90					95	
Glu	Met	Asp	Lys	Ala	Val	Ala	Ala	Val	Gln	Gln	Ala	Tyr	Leu	Ala	Tyr
			100					105					110		
Gln	Gln	Ala	Thr	Asp	Lys	Ala	Ala	Lys	Asp	Ala	Ala	Asp	Lys	Met	Ile
		115					120					125			
Asp	Glu	Ala	Lys	Lys	Arg	Glu	Glu	Glu	Ala	Lys	Thr	Lys	Phe	Asn	Thr
	130					135					140				
Val	Arg	Ala	Met	Val	Val	Pro	Glu	Pro	Glu	Gln	Leu	Ala	Glu	Thr	Lys
145				150					155				160		

Lys	Lys	Ser	Glu	Glu	Ala	Lys	Gln	Lys	Ala	Pro	Glu	Leu	Thr	Lys	Lys	
				165					170					175		
Leu	Glu	Glu	Ala	Lys	Ala	Lys	Leu	Glu	Glu	Ala	Glu	Lys	Lys	Ala	Thr	
			180					185					190			
Glu	Ala	Lys	Gln	Lys	Val	Asp	Ala	Glu	Glu	Val	Ala	Pro	Gln	Ala	Lys	
		195					200					205				
Ile	Ala	Glu	Leu	Glu	Asn	Gln	Val	His	Arg	Leu	Glu	Gln	Glu	Leu	Lys	
	210					215					220					
Glu	Ile	Asp	Glu	Ser	Glu	Ser	Glu	Asp	Tyr	Ala	Lys	Glu	Gly	Phe	Arg	
225					230					235					240	
Ala	Pro	Leu	Gln	Ser	Lys	Leu	Asp	Ala	Lys	Lys	Ala	Lys	Leu	Ser	Lys	
				245					250					255		
Leu	Glu	Glu	Leu	Ser	Asp	Lys	Ile	Asp	Glu	Leu	Asp	Ala	Glu	Ile	Ala	
			260					265					270			
Lys	Leu	Glu	Asp	Gln	Leu	Lys	Ala	Ala	Glu	Glu	Asn	Asn	Asn	Val	Glu	
		275					280					285				
Asp	Tyr	Phe	Lys	Glu	Gly	Leu	Glu	Lys	Thr	Ile	Ala	Ala	Lys	Lys	Ala	
	290					295					300					
Glu	Leu	Glu	Lys	Thr	Glu	Ala	Asp	Leu	Lys	Lys	Ala	Val	Asn	Glu	Pro	
305					310					315					320	
Glu	Lys	Pro	Ala	Pro	Ala	Pro	Glu	Thr	Pro	Ala	Pro	Glu	Ala	Pro	Ala	
				325					330					335		
Glu	Gln	Pro	Lys	Pro	Ala	Pro	Ala	Pro	Gln	Pro	Ala	Pro	Ala	Pro	Lys	
			340					345					350			
Pro	Glu	Lys	Pro	Ala	Glu	Gln	Pro	Lys	Pro	Glu	Lys	Thr	Asp	Asp	Gln	
		355					360					365				
Gln	Ala	Glu	Glu	Asp	Tyr	Ala	Arg	Arg	Ser	Glu	Glu	Glu	Tyr	Asn	Arg	
	370					375					380					
Leu	Thr	Gln	Gln	Gln	Pro	Pro	Lys	Ala	Glu	Lys	Pro	Ala	Pro	Ala	Pro	
385					390					395					400	
Lys	Thr	Gly	Trp	Lys	Gln	Glu	Asn	Gly	Met	Trp	Tyr	Phe	Tyr	Asn	Thr	
				405					410					415		
Asp	Gly	Ser	Met	Ala	Thr	Gly	Trp	Leu	Gln	Asn	Asn	Gly	Ser	Trp	Tyr	
			420					425					430			
Tyr	Leu	Asn	Ser	Asn	Gly	Ala	Met	Ala	Thr	Gly	Trp	Leu	Gln	Tyr	Asn	
		435					440					445				
Gly	Ser	Trp	Tyr	Tyr	Leu	Asn	Ala	Asn	Gly	Ala	Met	Ala	Thr	Gly	Trp	
	450					455					460					

Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met  
465 470 475 480

Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala  
485 490 495

Asn Gly Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr  
500 505 510

Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn  
515 520 525

Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp  
530 535 540

Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met  
545 550 555 560

Ala Thr Gly Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala  
565 570 575

Ser Gly Ala Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp  
580 585 590

Tyr Tyr Val Asn Gly Leu Gly Ala Leu Ala Val Asn Thr Thr Val Asp  
595 600 605

Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp Val  
610 615

<210> 2  
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<212> PRT  
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<223> stabilizing strand

<220>  
<221> MOD\_RES  
<222> (2)  
<223> Nle

<400> 2

Cys Xaa Gly Gly Gly Glu Ile Glu Ala Leu Lys Lys Glu Ile Glu Ala  
1 5 10 15

Leu Lys Lys Glu Ile Glu Ala Leu Lys Lys Glu Ile Glu Ala Leu Lys  
20 25 30

Lys Glu Ile Glu Ala Leu Lys Lys  
35 40

<210> 3  
<211> 38  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> hybrid sequence

<220>  
<221> MOD\_RES  
<222> (2)  
<223> Nle

<400> 3

Cys Xaa Gly Ile Glu Glu Leu Glu Lys Lys Ile Thr Glu Leu Lys Gln  
1 5 10 15

Lys Ile Asp Ala Leu Glu Asn Gln Ile His Arg Leu Glu Gln Glu Ile  
20 25 30

Lys Glu Leu Asp Glu Ser  
35

<210> 4  
<211> 38  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> hybrid sequence

<220>  
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<222> (2)  
<223> Nle

<400> 4

Cys Xaa Gly Leu Glu Glu Ala Glu Lys Lys Ala Thr Glu Ala Lys Gln  
1 5 10 15

Lys Val Asp Ala Leu Glu Asn Gln Val His Arg Leu Glu Gln Glu Leu  
20 25 30

Lys Glu Ile Asp Glu Ser  
35

<210> 5  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> consensus sequence

<220>

<221> PEPTIDE  
<222> (4)..(20)  
<223> Amino acids 4, 5, 12, 16 and 20 are Xaa wherein Xaa = any amino acid

<400> 5

Glu Glu Leu Xaa Xaa Lys Ile Asp Glu Leu Asp Xaa Glu Ile Ala Xaa  
1 5 10 15

Leu Glu Lys Xaa  
20

<210> 6  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> consensus sequence

<400> 6

Glu Glu Leu Ser Asp Lys Ile Asp  
1 5

<210> 7  
<211> 27  
<212> PRT  
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<223> hybrid sequence

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<222> (2)  
<223> Nle

<400> 7

Cys Xaa Gly Glu Ile Glu Ala Leu Lys Lys Lys Ile Glu Glu Leu Ser  
1 5 10 15

Asp Lys Ile Asp Glu Leu Glu Lys Glu Ile Lys  
20 25

<210> 8  
<211> 21  
<212> PRT  
<213> Haemophilus influenzae

<400> 8

Ile Lys Lys Val Leu Glu Ile Gly Leu Asn Met Ser Gln Glu Ala Ser  
1 5 10 15

Asn Leu Thr Ser Ala  
20

<210> 9  
<211> 27  
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<223> hybrid sequence

<400> 9

Glu Ala Glu Ile Lys Lys Leu Leu Glu Ile Ile Leu Asn Leu Ser Gln  
1 5 10 15

Glu Ile Ser Asn Leu Thr Ser Ala Leu Lys Gly  
20 25

<210> 10  
<211> 20  
<212> PRT  
<213> Streptococcus pneumoniae

<400> 10

Leu Glu Lys Asp Val Glu Asp Phe Lys Asn Ser Asp Gly Glu Gln Ala  
1 5 10 15

Glu Gln Val Leu  
20

<210> 11  
<211> 15  
<212> PRT  
<213> Streptococcus pneumoniae

<400> 11

Leu Glu Asp Asn Leu Lys Asp Ala Glu Thr Asn Asn Val Glu Asp  
1 5 10 15

<210> 12  
<211> 10  
<212> PRT  
<213> Streptococcus pneumoniae

<400> 12

Leu Ala Lys Lys Gln Thr Glu Leu Glu Lys  
1 5 10

<210> 13  
<211> 35  
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<213> Artificial Sequence

<220>

<223> hybrid sequence

<400> 13

Asp Val Glu Asp Phe Lys Asn Ser Asp Gly Glu Leu Glu Asp Asn Leu  
1 5 10 15

Lys Asp Ala Glu Thr Asn Asn Val Glu Asp Ala Lys Lys Gln Thr Glu  
20 25 30

Leu Glu Lys  
35

<210> 14

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> hybrid sequence

<400> 14

Asp Ile Glu Asp Leu Lys Asn Ser Ile Gly Glu Leu Glu Asp Asn Ile  
1 5 10 15

Lys Glu Leu Glu Thr Asn Ile Val Glu Leu Ala Lys Lys Ile Thr Glu  
20 25 30

Leu Glu Lys  
35

<210> 15

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Coiled-coil scaffold

<220>

<221> PEPTIDE

<222> (1)

<223> Amino acid 1 is Xaa wherein Xaa = A and A can be I, L or V.

<220>

<221> PEPTIDE

<222> (2)..(7)

<223> Amino acids 2, 3, 5-7 are Xaa wherein Xaa = any amino acid.

<220>

<221> PEPTIDE

<222> (4)

<223> Amino acid 4 is Xaa wherein Xaa = D and D can be I, L or V.

<220>

<221> PEPTIDE  
<222> (1)..(7)  
<223> Amino acids 1-7 can be repeated one or more times.

<400> 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5

<210> 16  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Coiled-coil scaffold

<220>  
<221> MOD\_RES  
<222> (2)  
<223> Nle

<220>  
<221> PEPTIDE  
<222> (5)..(10)  
<223> Amino acids 5, 6, and 8-10 are Xaa wherein Xaa = any amino acid.

<220>  
<221> PEPTIDE  
<222> (4)..(10)  
<223> Amino acids 4-10 can be repeated one or more times.

<400> 16

Cys Xaa Gly Ile Xaa Xaa Leu Xaa Xaa Xaa  
1 5 10

<210> 17  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> linear sequence

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Glu Glu Glu Ser Asp Lys Lys Asp Glu Glu Asp Ala Glu Lys Ala Glu  
1 5 10 15